

<110> THE HORTICULTURE AND FOOD RESEARCH INSTITUTE OF NEW ZEALAND LIMITED

<120> ENZYMES AND POLYNUCLEOTIDES ENCODING THE SAME

<130> 497047 KXR

<150> NZ 523384

<151> 2002-12-24

<160> 16

<170> PatentIn version 3.1

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<211> 2019

<212> DNA

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PCTNZ2003000294 seq.txt

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His Pro Ser Ile Trp Gly Asp His Phe Leu Ala Tyr Ser Ser Asp Ala
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Leu Lys Gln Lys Val Arg Lys Met Leu Glu Ala Ala Ala Glu Gln Ser
65 70 75 80

Ser Gln Met Leu Asn Leu Val Asp Lys Ile Gln Arg Leu Gly Val Ser
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Tyr His Phe Glu Thr Glu Ile Glu Thr Ala Leu Arg His Ile Tyr Lys
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Thr Cys Asp Tyr His Phe Asp Asp Leu His Thr Ala Ala Leu Ser Phe
115 120 125

Arg Leu Leu Arg Gln Gln Gly Tyr Pro Val Ser Cys Asp Met Phe Asp
130 135 140

Lys Phe Lys Asn Ser Lys Gly Glu Phe Gln Glu Ser Ile Ile Ser Asp
145 150 155 160

Val Gln Gly Met Leu Ser Leu Tyr Glu Ala Thr Cys Leu Arg Ile His
165 170 175

Gly Glu Asp Ile Leu Asp Glu Ala Leu Ala Phe Thr Ile Thr Gln Leu
180 185 190

Arg Ser Ala Leu Pro Asn Leu Ser Thr Pro Phe Lys Glu Gln Ile Ile
195 200 205

His Ala Leu Asn Gln Pro Ile His Lys Gly Leu Thr Arg Leu Asn Ala
210 215 220

Arg Ser His Ile Leu Phe Phe Glu Gln Asn Asp Cys His Ser Lys Asp
225 230 235 240

Leu Leu Asn Phe Ala Lys Leu Asp Phe Asn Leu Leu Gln Lys Leu His
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260 265 270

PCTNZ2003000294 seq.txt

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Asp Val Tyr Gly Thr Leu Glu Glu Leu Val Leu Phe Thr Asp Ala Ile
325 330 335

Glu Arg Trp Glu Ile Ser Ala Leu Asp Gln Leu Pro Glu Tyr Met Lys
340 345 350

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Met Ala Lys Gln Gly Arg Ser Tyr Cys Val Asp Tyr Ala Lys Ser Ser
370 375 380

Met Lys Ile Leu Val Arg Ala Tyr Phe Glu Glu Ala Lys Trp Phe His
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Ile Val Gln Ala Ala Ser Val Ile Gly Arg Leu Lys Asp Asp Ile Val
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Ser Met Pro Ile Asn
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PCTNZ2003000294 seq.txt

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PCTNZ2003000294 seq.txt

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<212> PRT

<213> Actinidia deliciosa

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His Pro Ser Ile Trp Gly Asp His Phe Leu Ala Tyr Ser Ser Asp Ala
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60

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Ser Gln Met Leu Asn Leu Val Asp Lys Ile Gln Arg Leu Gly Val Ser
 85 90 95

Tyr His Phe Glu Thr Glu Ile Glu Thr Ala Leu Arg His Ile Tyr Lys
 100 105 110

Thr Cys Asp Tyr His Phe Asp Asp Leu His Thr Ala Ala Leu Ser Phe
 115 120 125

Arg Leu Leu Arg Gln Gln Gly Tyr Pro Val Ser Cys Asp Met Phe Asp
 130 135 140

Lys Phe Lys Asn Ser Lys Gly Glu Phe Gln Glu Ser Ile Ile Ser Asp
 145 150 155 160

Val Arg Gly Met Leu Ser Leu Tyr Glu Ala Thr Cys Leu Met Ile His
 165 170 175

Gly Glu Asp Ile Leu Asp Glu Ala Leu Ala Phe Thr Ile Thr Gln Leu
 180 185 190

Arg Ser Ala Leu Pro Asn Leu Ser Thr Pro Phe Lys Glu Gln Ile Ile
 195 200 205

His Ala Leu Asn Gln Pro Ile His Lys Gly Leu Thr Arg Leu Asn Ala
 210 215 220

Arg Ser His Ile Leu Phe Phe Glu Gln Asn Asp Cys His Ser Lys Asp
 225 230 235 240

Leu Leu Asn Phe Ala Lys Leu Asp Phe Asn Leu Leu Gln Lys Leu His
 245 250 255

Gln Arg Glu Leu Cys Glu Ile Thr Arg Glu Ile Ser Ala Leu Asp Gln
 260 265 270

Leu Pro Glu Tyr Met Lys Leu Cys Tyr Gln Ala Leu Leu Asp Val Tyr
 275 280 285

Ser Met Ile Asp Glu Glu Met Ala Lys Gln Gly Arg Ser Tyr Cys Val
 290 295 300

PCTNZ2003000294 seq.txt

Asp Tyr Ala Lys Ser Ser Met Lys Ile Leu Val Arg Ala Tyr Phe Glu
305 310 315 320

Glu Ala Lys Trp Phe His Gln Gly Tyr Val Pro Thr Met Glu Glu Tyr
325 330 335

Met Gln Val Ala Leu Val Thr Ala Gly Tyr Lys Met Leu Ala Thr Ser
340 345 350

Ser Phe Val Gly Met Gly Glu Leu Ala Thr Lys Glu Ala Phe Asp Trp
355 360 365

Val Ser Asn Asp Pro Leu Ile Val Gln Ala Ala Ser Val Ile Gly Arg
370 375 380

Leu Lys Asp Asp Ile Val Gly His Lys Phe Glu Gln Lys Arg Gly His
385 390 395 400

Val Ala Ser Ala Val Glu Cys Tyr Ser Lys Gln His Gly Thr Thr Glu
405 410 415

Glu Glu Ala Ile Ile Glu Leu Tyr Lys Gln Val Thr His Ser Trp Lys
420 425 430

Asp Met Asn Ala Glu Cys Leu Cys Pro Thr Lys Val Pro Met Pro Leu
435 440 445

Leu Ala Arg Val Leu Asn Leu Ala Arg Val Leu Tyr Val Ile Tyr Gln
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<213> Actinidia deliciosa

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 His Pro Ser Ile Trp Gly Asp His Phe Leu Ala Tyr Ser Ser Asp Ala
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 50 55 60
 Leu Lys Gln Lys Val Arg Lys Met Leu Glu Ala Ala Ala Lys Gln Ser
 65 70 75 80
 Ser Gln Met Leu Asn Leu Val Asp Lys Ile Gln Arg Leu Gly Val Ser
 85 90 95
 Tyr His Phe Glu Thr Glu Ile Glu Thr Ala Leu Arg His Ile Tyr Lys
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 Thr Cys Asp Tyr His Phe Asp Asp Leu His Thr Ala Ala Leu Ser Phe
 115 120 125
 Arg Leu Leu Arg Gln Gln Gly Tyr Pro Val Ser Cys Asp Met Phe Gly
 130 135 140
 Lys Phe Lys Asn Cys Lys Gly Glu Phe Gln Glu Ser Ile Ile Ser Asp
 145 150 155 160
 Val Arg Gly Met Leu Ser Leu Tyr Glu Ala Thr Cys Leu Arg Ile Arg
 165 170 175
 Gly Glu Asp Ile Leu Asp Glu Ala Leu Ala Phe Thr Thr Thr Gln Leu
 180 185 190
 Gln Ser Ala Leu Pro Asn Leu Ser Thr Pro Ile Lys Glu Gln Ile Ile
 195 200 205
 His Ala Leu Asn Gln Pro Ile His Lys Trp Leu Thr Arg Leu Asp Ala
 210 215 220
 Arg Arg His Ile Leu Phe Phe Glu Gln Asn Asp Cys His Gly Lys Asp
 225 230 235 240
 Leu Leu Asn Phe Ala Lys Leu Asp Phe Asn Ser Leu Gln Lys Leu His
 245 250 255
 Gln Arg Glu Leu Cys Glu Ile Thr Arg Trp Trp Lys Asp Leu Asp Phe
 260 265 270

PCTNZ2003000294 seq.txt

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Trp Ile₂₉₀ Leu Gly Val Tyr Phe₂₉₅ Glu Pro Gln Tyr Leu₃₀₀ Arg Ala Arg Arg

Met₃₀₅ Leu Thr Lys Val Ile₃₁₀ Ala Leu Thr Ser Ile₃₁₅ Ile Asp Asp Ile Tyr₃₂₀

Asp Val Tyr Gly Thr₃₂₅ Leu Glu Glu Leu Val₃₃₀ Leu Phe Thr Asp Ala₃₃₅ Ile

Glu Arg Trp Glu₃₄₀ Ile Ser Ala Leu Asp₃₄₅ Asn Leu Pro Asp Tyr₃₅₀ Met Lys

Leu Cys Tyr₃₅₅ Gln Ala Leu Leu Asp₃₆₀ Val Tyr Ser Met Ile₃₆₅ Asp Glu Glu

Met Ala₃₇₀ Lys Gln Gly Arg Ser₃₇₅ Tyr Cys Val Asp Tyr₃₈₀ Ala Lys Ser Ser

Met₃₈₅ Lys Ile Leu Val Arg₃₉₀ Ala Tyr Phe Glu Glu₃₉₅ Ala Lys Trp Phe His₄₀₀

Gln Gly Tyr Val Pro₄₀₅ Thr Met Glu Glu Tyr₄₁₀ Met Gln Val Ala Leu Val₄₁₅

Thr Ala Gly Tyr₄₂₀ Lys Met Leu Ala Thr₄₂₅ Ser Ser Phe Val Gly₄₃₀ Met Gly

Glu Leu Ala₄₃₅ Thr Lys Glu Ala Phe₄₄₀ Asp Trp Val Ser Asn₄₄₅ Asp Pro Leu

Ile Val₄₅₀ Gln Ala Ala Ser Val₄₅₅ Ile Gly Arg Leu Lys₄₆₀ Asp Asp Ile Val

Gly His Lys Phe Glu Gln₄₇₀ Lys Arg Gly His Val₄₇₅ Ala Ser Ala Val Glu₄₈₀

Cys Tyr Ser Lys Gln₄₈₅ His Gly Thr Ile Glu₄₉₀ Glu Glu Ala Ile Ile Glu₄₉₅

Leu Asp Lys Gln₅₀₀ Val Thr His Ser Trp₅₀₅ Lys Asp Ile Asn Ala₅₁₀ Glu Cys

Leu Cys Pro Ile Lys Val Pro Met Pro Leu Leu Ala Arg Val Leu Asn

515

Leu Ala Arg Val Leu Tyr Val Ile Tyr Gln Asp Glu Asp Gly Tyr Thr
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Ser Met Pro Ile Asn
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<212> DNA

<213> Actinidia chinensis

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<213> Actinidia chinensis

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Glu Glu Tyr Met Gln Val Ala Ile Val Thr Gly Ala Tyr Lys Ile Leu
35 40 45

Ala Thr Thr Ser Phe Val Gly Met Gly Glu Leu Ala Thr Lys Glu Val
50 55 60

Phe Asp Trp Val Ser Asn Asp Pro Leu Ile Val Gln Ala Ala Ser Ile
65 70 75 80

Val Ser Arg Leu Thr Asp Asp Ile Val Gly His Lys Phe Glu Gln Lys
85 90 95

Arg Gly His Val Ala Ser Ala Val Glu Cys Tyr Met Lys Gln His Gly
100 105 110

Thr Thr Glu Glu Glu Ala Ile Val Glu Leu Tyr Lys Gln Val Thr Asn
115 120 125

Ala Trp Lys Asp Met Asn Ala Glu Cys Leu Phe Pro Thr Lys Val Pro
130 135 140

Met Pro Leu Leu Val Arg Val Leu Asn Leu Ala Arg Val Ile Asn Val
145 150 155 160

Leu Tyr Lys Asp Glu Asp Gly Tyr Thr His Ser Arg Thr Lys Val Lys
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Lys Phe Val Thr Ser Val Leu Val Asp Phe Val Pro Ile Ser
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<211> 755

<212> DNA

<213> Vaccinium corymbosum

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PCTNZ2003000294 seq.txt

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Val Ser Ser Asp Pro Leu Ile Val Glu Ala Ala Ser Val Ile Cys Arg
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Leu Met Asp Asp Met Ala Gly His Lys Phe Glu Gln Glu Arg Gly His
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Val Ala Ser Ala Val Glu Cys Tyr Met Lys Gln His Gly Ala Thr Gln
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Glu Val Val Leu Leu Glu Phe Lys Lys Arg Val Thr Asn Ala Trp Lys
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PCTNZ2003000294 seq.txt

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